# ISOLATION OF TRISOMICS AND TETRASOMICS IN GUAVA (*PSIDIUM GUAJAVA* L.)

P. K. MAJUMDER AND S. K. MUKHERJEE*

*Division of Horticulture, Indian Agricultural Research Institute, New Delhi-12, India*

THE study of aneuploidy has been widely appreciated for its great value in fundamental genetics, especially the monosomics, nullisomics and trisomics. The pioneer investigation on *Datura* by Blakeslee and Belling,[1] has stimulated many studies on annual crop plants, but no systematic approach has yet been made in tree fruits, particularly in guava. The present investigation was, therefore, undertaken to isolate trisomics and tetrasomics, which may be useful in studying cytogenetics of guava and in evolving guava with reduced seed number due to chromosome imbalance.

The plant materials were raised from seeds of open-pollinated triploid and crosses between the triploid ($3n = 33$) and diploid. The seeds were grouped into very big, big, medium and small classes on weight basis, and the seedlings were planted in 1963, whose chromosome numbers were determined from shoot and root tip squashes.

"Very big" seeds yielded 78% hypo- and hyper-triploid; "big seeds" gave 50% aneuploids with somatic chromosome numbers between 27 and 32, and only 17% from "medium-sized" seeds. "Small seed," on the other hand, yielded 88% aneuploids, which were mostly trisomics and tetrasomics.

Eight morphologically distinct trisomics were identified from the polygraphs (Fig. 1) adopting Hutchinson's technique in *Xanthium*.[2] Twelve distinctive vegetative characters were chosen for plotting polygraph which gave a simultaneous expression of different variable characters, which were further confirmed from the karyological analysis of different trisomics, where extra chromosome was morphologically distinct. The trisomics were mostly reduced in vigour in comparison to diploid sibs, with pollen sterility of 5 to 24%. At Metaphase I of meiosis, $11_{II} + 1_{I}$ association was more frequently observed (52-95%) than $10_{II} + 1_{III}$. The 11-12 distribution in Anaphase I was observed in 72 to 98% of PMcs (Fig. 2).

Out of 20 plants in 24-chromosome group, 17 were morphologically distinct. On the basis of chromosome association at Metaphase I and phenotypic appearance, 10 tetrasomics and 5 double trisomics were identified. The meiosis of remaining 5 plants could not be studied as they did not flower. The tetrasomics were usually shorter than the trisomics. Leaf size was most affected in the tetrasomics, with varying Metaphase I chromosomes association

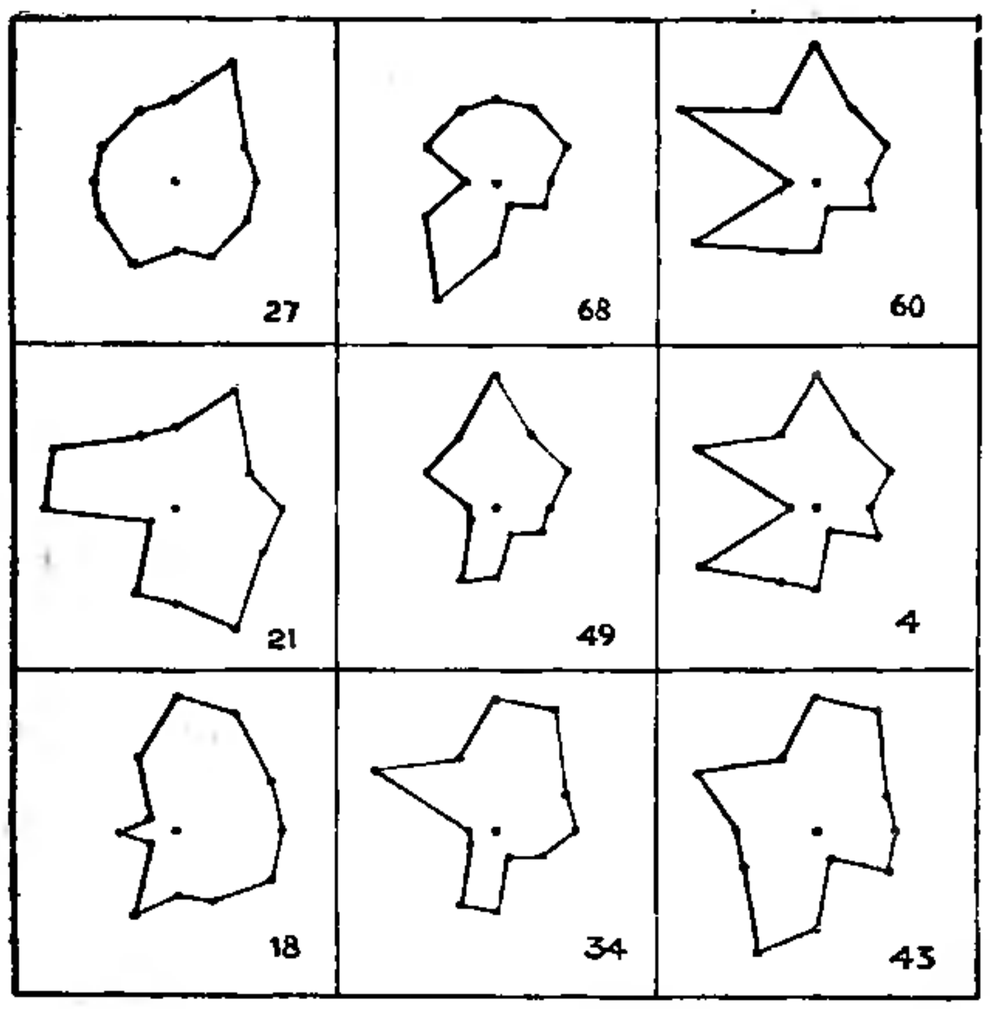


FIG. 1. Polygraphs of trisomics ($2n + 1$).

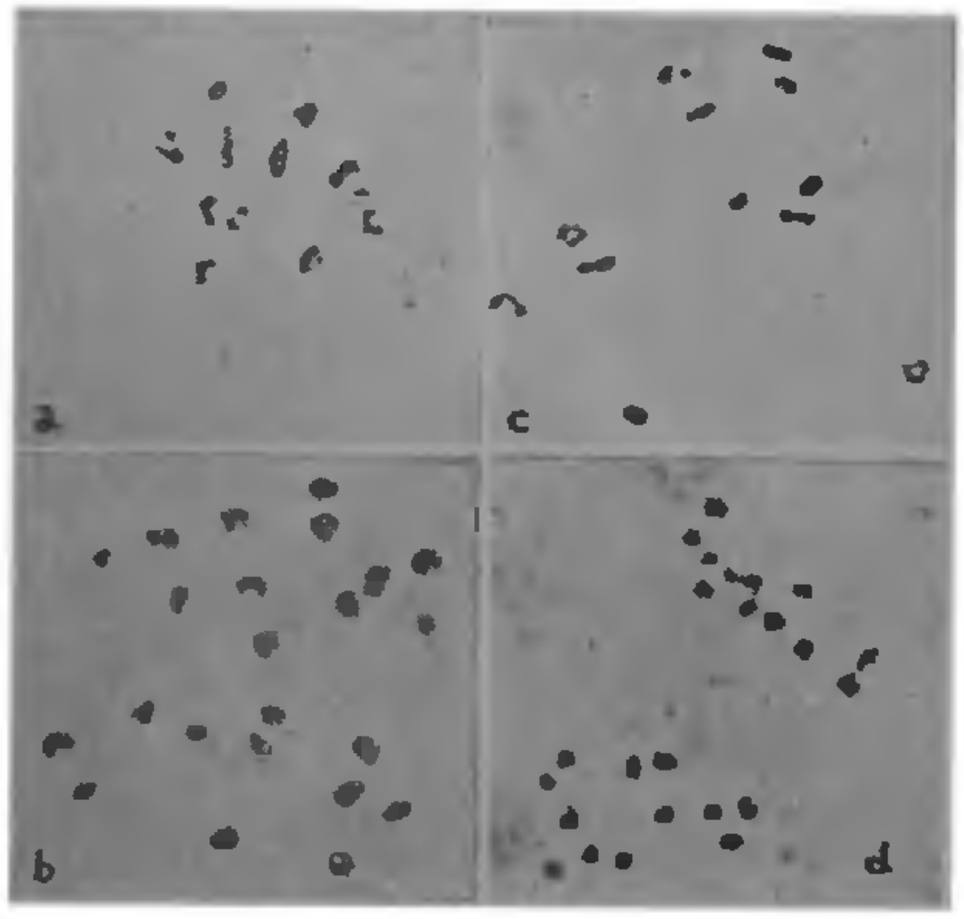


FIG. 2. (*a*) $2n + 1$ Metaphase $11_{II} + 1$, × 2,572. (*b*) $2n + 1$ Anaphase 11-12 distribution, × 2,695. (*c*) $2n + 2$ Metaphase $12_{II}$, × 2,572. (*d*) $2n + 2$ Anaphase 12-12 distribution, × 2,572.

* At present, Director, Botanical Survey of India, 14, Madan Street, Calcutta-13.

(Fig. 2). The pollen sterility was higher in tetrasomics than trisomics. Two tetrasomic types had fruits with normal size and shape, with much reduced seed size (75%) and the seed number of each fruit was half of the diploid cultivar.

Fruit shape was mostly deformed in hyper-triploid, hypo-triploid and triploid types, probably because of high ovule sterility. It was found that tolerable limit of extra chromosome in case of guava was four, beyond this limit seed fertility and fruit shape was found to be adversely affected.

As guava is vegetatively propagated, the aneuploid types can very well be maintained, unlike annual crop plants. The addition of two chromosomes to diploid number has shown a great promise in guava improvement. This method of breeding can very well be adopted in tree fruits where numerous seeds decrease the fruit value.

1. Blakeslee, A. F. and Belling, J., *Amer. Nat.*, 1924, **56**, 16.
2. Love, D. and Nadeau, L., *Canad. J. Genet. Cyt.*, 1961, **3**, 289.

## A NOTE ON THE CYTOGENETIC STATUS OF *NICOTIANA AMPLEXICAULIS* BURBIDGE

D. M. GOPINATH, K. V. KRISHNAMURTHY AND A. S. KRISHNAMURTHY
*Central Tobacco Research Institute, Rajahmundry, A.P.*

WHILE assigning taxonomical positions for the five new Australian species of *Nicotiana*, Burbidge (1960) fixed *N. amplexicaulis* ($2n = 36$) between *N. gossei* ($2n = 36$) and *N. maritima* ($2n = 32$). Morphologically, *N. amplexicaulis* may well be regarded as a mini copy of *N. gossei* but bears little resemblance to *N. maritima*. Distributionally, the three species are widely separated, *N. gossei* in Central Australia, *N. amplexicaulis* in Queensland and *N. maritima* in South Australia. According to Goodspeed (1954) almost all the Australian species had their origin through amphidiploidy followed by chromosomal and genetic reorganisation. Aneuploidy through loss of chromosomes played an important part in the evolution of the Australian species in particular. In this context, the cytogenetic position of *N. amplexicaulis* was investigated to determine its relationship to the older species. For this purpose, inter- and intrasectional crosses between *N. amplexicaulis* and certain species of *Nicotiana* were done and the cytology of the hybrids followed. Since *N. amplexicaulis* is similar to *N. gossei* in chromosome number and also in morphology, comparison of chromosome behaviour of crosses between *N. gossei* and the same species involved in *N. amplexicaulis* crosses was made. The trend of cytogenetic behaviour of *N. gossei* and *N. amplexicaulis* is almost similar.

The chromosome pairing of *N. gossei* and *N. amplexicaulis* is given in Table I. From Table I it may be seen that a high degree of pairing between *N. amplexicaulis* as well as *N. gossei* with the species is evident. This points to a close genotypic homology between *N. gossei* and *N. amplexicaulis*. This is further proved by the complete pairing and fertility of the hybrids between the two species. The pairing relationship between *N. amplexicaulis* and the other species, as listed in Fig. 1,

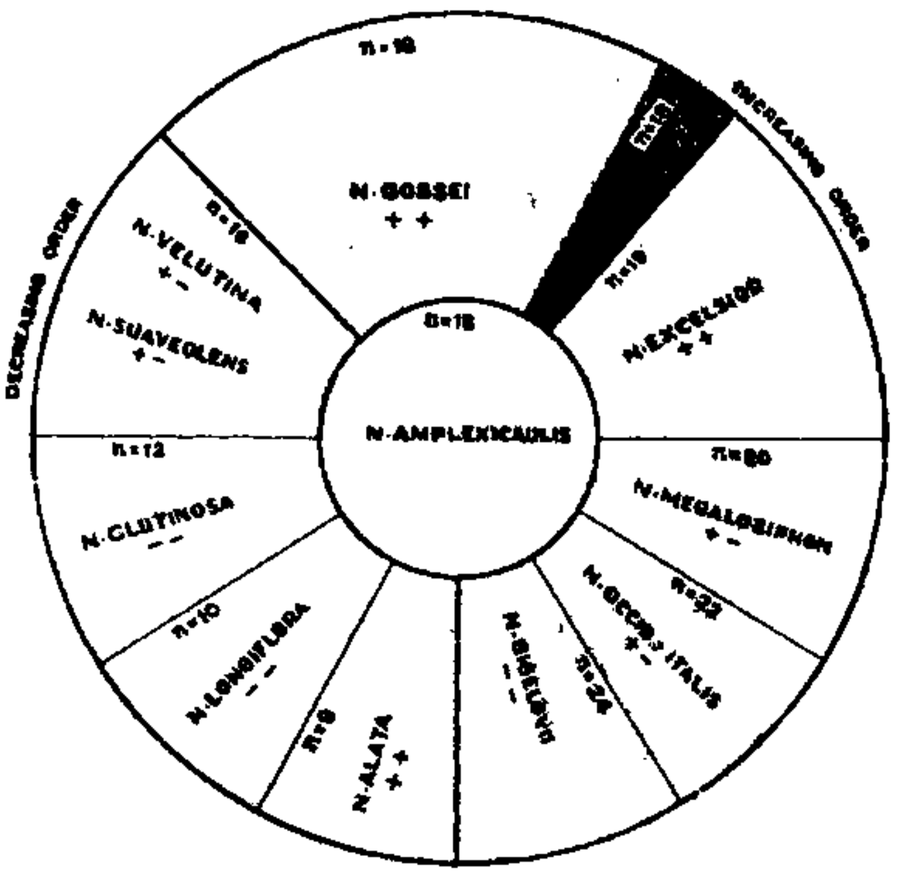


FIG. 1. Chart indicating *N. amplexicaulis* crosses with other species of *Nicotiana*. + indicates goodness and − indicates failure. First symbol for chromosome pairing and second symbol for pollen and seed fertility. The striped portion will be the cytogenetic location for *N. amplexicaulis*.